SEQ ID NO:1

GCCCTGCCTGCCCTGCCTGCCCTGCCTGCCCTGCCTGCCCTGCCTGCCCTGCCTGCCCTGCCTGCC
CTGCCTCAGGAATCCCAGAACGAAGGCCTGGCCTGGGCCTTCCTGGCCATGGCTCCCTCAGTCCTCTGGGCACCA
CAAAGGCTTTTTCCCAGGAAGAGAACGCCTTGCCTCTACTTGTAGCTGGGGTTGCCTGGGAGGTGCGTCATAGTG
TGTCTTAGTAAGTTTTGAACACTGGGGAAGAGCCTCAGGCGTCTCTACGCGGGTAGTGTCAGTGCTGACCCTTTG
AAAGTGGTGTGTTCCCTTCTGAGGGATGTGCCTGTGGTGAACTCTTCAGGAGAGCTGCCCCAGGGAAGGACAGGA
CAGATGTCTTTTAAACACCAGGGAAAGTACACAGCCTCCCGCCTCAGGCGGAGCCCAGTGGAAAGTAGCCACCTT
CCTTGCAATCTGCCACACCTGGCACAGGAGAGCCTGCACTGGCCGCGTTGGGCTTTGGTGCTGGCTCTGTACTCC
CACTTGCTTGCTGGTGGCCTCANGGAAAGGTCATCTCTNAANGAAACAAAGCCACCTNCTCCCCCTCCCTGGCAT
GCNTTTTTCNGCCCACAGCCCCGTGTGTGCCAACANAAATTTTGGCNNCANGANGNAAGGNTGGGANANAACCCN
AAAACTATTGTGGCTNCCCTGTTGCCCCTGCTGTNCCNGGTTTNATGGGAACGAGGNCCTCCCACCCCCTNGGNA
ACGNATAACCNCACCCGTGGNAATGGNGGGNTTGGGGTGCANTCNTTACCCNCCCCANGGGNNAGGGCGGGGGNT
CAAACCTNGGGGAACNNAAAAAAAAACCCANGGCCNTTTGNGTCCNCNNNGGCCCCNAGGGNTTTTATTTTNTTT
ANAANGGGANGGTGNCCCCAATNCTCNNAAAACTNGGNTTTTTTAAGNNTTTCTTGCAAAATTGNN

FIG. 1A

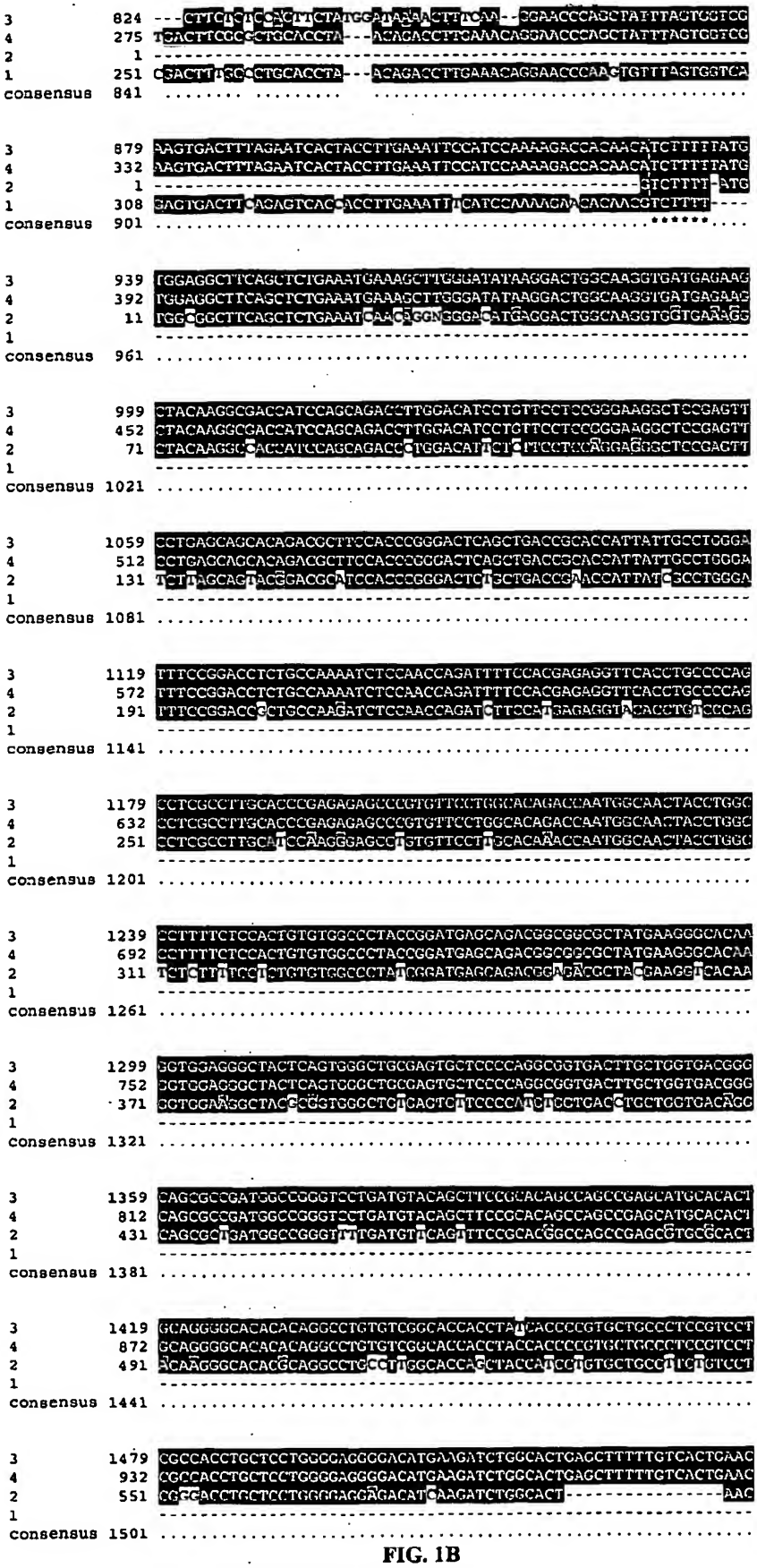

FIG. 1B

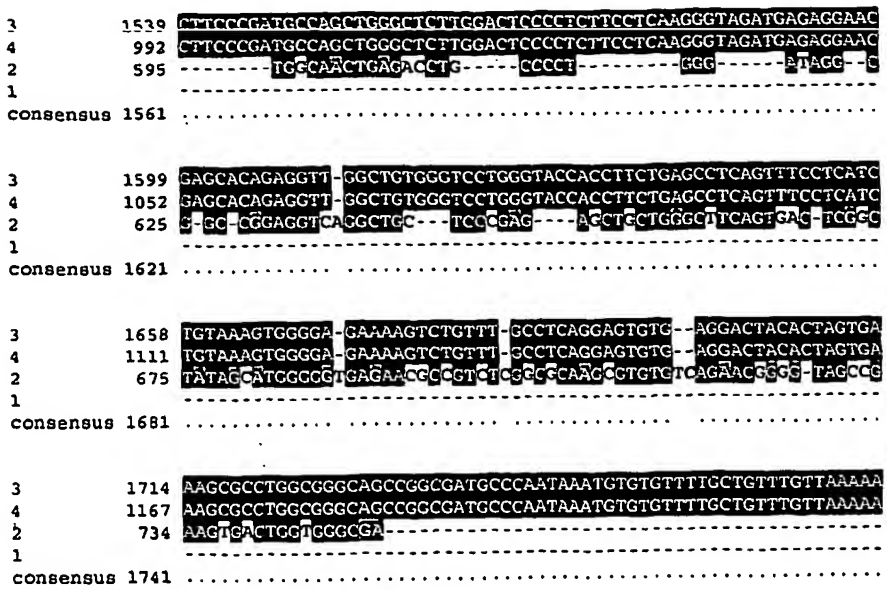

FIG. 1B (continued)

SEQ ID NO:2

GAGGGGTGGACCAAGAGCTTCCGTGTGTGTGTGTGTGTGGAAGTCACCTTTGTGTGACTGTATGGCCTCGCTGGT
GGCATATGATGATTCTGACTCCGAGACCGAGGCTGACCCTGCCAGAAGTGGGGACGCTGCAGGTGTGGAATGCTG
TGGACTCGGGACACTGCCTGCAGACCTACTCTGTGCACAGTGAGGCAGTAAGGGCTGAACGGTGGTCTCCCTGTG
GCCGGCGCATCCTCAGTGGTGGCTTCGACTTTGCCCTGCACCTAACAGACCTTGAAACAGGAACCCAAGTGTTTA
GTGGTCAGAGTGACTTCAGAGTCACCACCTTGAAATTTCATCCAAAAGAACACAACGTCTTTTtATGTGGCGGCT
TCAGCTCTGAAATCAACAGGNGGGACATGAGGACTGGCAAGGTGGTGAAAGGCTACAAGGCCACCATCCAGCAGA
CCCTGGACATTCTCTTCCTCCAGGAGGGCTCCGAGTTTCTTAGCAGTACGGACGCATCCACCCGGGACTCTGCTG
ACCGAACCATTATCGCCTGGGATTTCCGGACCGCTGCCAAGATCTCCAACCAGATCTTCCATGAGAGGTACACCT
GTCCCAGCCTCGCCTTGCATCCAAGGGAGCCTGTGTTCCTTGCACAAACCAATGGCAACTACCTGGCTCTCTTTT
CCTCTGTGTGGCCCTATCGGATGAGCAGACGGAGACGCTACGAAGGTCACAAGGTGGAAGGCTACGCGGTGGGCT
GTGAGTGTTCCCCATGTGGTGACCTGCTGGTGACAGGCAGCGCTGATGGCCGGGTTTTGATGTTCAGTTTCCGCA
CGGCCAGCCGAGCGTGCGCACTACAAGGGCACACGCAGGCCTGCCTTGGCACCAGCTACCATCCTGTGCTGCCTT
CTGTCCTCGGGACCTGCTCCTGGGGAGGAGACATCAAGATCTGGCACTAACTGGCAACTGAGACCTGCCCCTGGG
ATAGGCGGCCGGAGGTCAGGCTGCTCCCGAGAGCTGCTGGGCTTCAGTGACTCGGCTATAGCATGGGGGTGAGAA
CGCCGTCTCGGCGCAAGCGTGTGTCAGAACGGGGTAGCCGAAGTGACTGGTGGGCGA

FIG. 2A

SEQ ID NO:3

MMILTPRPRLTLPEVGTLQVWNAVDSGHCLQTYSVHSEAVRAERWSPCGRRILSGGFDFALHLTDLETGTQVFSG
QSDFRVTTLKFHPKEHNVFLCGGFSSEINRXDMRTGKVVKGYKATIQQTLDILFLQEGSEFLSSTDASTRDSADR
TIIAWDFRTAAKISNQIFHERYTCPSLALHPREPVFLAQTNGNYLALFSSVWPYRMSRRRRYEGHKVEGYAVGCE
CSPCGDLLVTGSADGRVLMFSFRTASRACALQGHTQACLGTSYHPVLPSVLGTCSWGGDIKIWH

FIG. 2B

Exon 1
SEQ ID NO:4

ATGACAGGCTGGGTGGGCGGCGCCGCCGCAGCCTCCCGGTCCCTCGTGGT
ACAGGTGCCCAGAGAACAGACAGCCCGGTTCCGAGCTGGATCCTCGGGGC
GCGGCGCCGGGGCGTCAACCGAAGGCCCCGGCGCCACCTCGGCATCCCTC
CCTCGCTCCCGGCGCAGTGACCACCCCCTCCTCACTTACCGGCGGCCCCC
ACTTCGGCCCCACCAGTCAGCACCCCCAAGTTCAGCCACCGGTACCTCTT
GGGCGTCCGTGGAAACACCAGCCGGCTGGAATAACTTCCG

Exon 2
SEQ ID NO:5

GAAGTCACCTTTGTGTGACTGTATGGCCTCGCTGGTGGCATATGATGATT
CTGACTCCGAGACCGAGGCTGACCCTGCCAGAAGTGGGGACGCTGCAG

Exon 3
SEQ ID NO:6

CTGCCTGTCTTAAGCCACTAAAACCTGCCTGG
GACGTCCTCAAACCTTCTCATGATCAAAGCACATTTGAAAGCACAGCTGG
AAATGCCAGCTCTTCTCAGAGGAAAAGGGGTGAGGACTGTGTGCTTCCCT
ATATCCCCAAGAGGCTAAGGCAGCTGCAAGCGCTGAATCCAGAAGCAG

Exon 4
SEQ ID NO:7

TGTCTGAGTTCATCCAGCCATATTTGA
ACAGTCAGTACAGAGAGACTACGGTCCCCAAGAAAGTGCTTTTCCACCTT
CGAGGCCACAGGGGCCCGGTCAACAGCATTCAGTGGTGTCCAGTCTTTTG
CAAGAGCCACATGCTTCTCTCTGCTTCCATGGACAAAACCTTCAAG

Exon 5
SEQ ID NO:8

TTCTGCCGTGAACATGGCTATGCA
GGCACCTCTGTGGATCCCGACACAGGCTCCTTTGGGATGGACCCAG

Exon 6
SEQ ID NO:9

GAATCC
CAGAACGAAGGCCTGGCCTGGGCCTTCCTGGCCATGGCTCCCTCAGTCCT
CTGGGCACCACAAAGGCTTTTTCCCAGGAAGAGAACGCCTTGCCTCTACT
TGTAGCTGGGGTTGCCTGGGAG

FIG. 2C

SEQ ID NO:10

ggcacgagggagggaggaggtgagagtgattagtgggagaagaaaagcaggcccaggaccaagccctggggactg
gggacatcctcggtgaccctgtggagcattgagccatgccagctctgtgcctggtgctgtgctggtttcaagggc
tgttgggagaggtatggaacgccgtggactccgggcactgcctgcagacctactccctgcacacagaggcagtgc
gggccgcccggtgggctccctgtggccggcgcatcctcagtggtggctttgacttcgcgctgcacctaacagacc
ttgaaacaggaacccagctatttagtggtcgaagtgactttagaatcactaccttgaaattccatccaaaagacc
acaacatctttttatgtggaggcttcagctctgaaatgaaagcttgggatataaggactggcaaggtgatgagaa
gctacaaggcgaccatccagcagaccttggacatcctgttcctccgggaaggctccgagttcctgagcagcacag
acgcttccacccgggactcagctgaccgcaccattattgcctgggatttccggacctctgccaaaatctccaacc
agattttccacgagaggttcacctgccccagcctcgccttgcacccgagagagcccgtgttcctggcacagacca
atggcaactacctggccctttctccactgtgtggccctaccggatgagcagacggcggcgctatgaagggcaca
aggtggagggctactcagtgggctgcgagtgctccccaggcggtgacttgctggtgacgggcagcgccgatggcc
gggtcctgatgtacagcttccgcacagccagccgagcatgcacactgcaggggcacacacaggcctgtgtcggca
ccacctaccaccccgtgctgccctccgtcctcgccacctgctcctggggagggacatgaagatctggcactgag
ctttttgtcactgaaccttcccgatgccagctgggctcttggactcccctcttcctcaagggtagatgagaggaa
cgagcacagaggttggctgtgggtcctgggtaccaccttctgagcctcagtttcctcatctgtaaagtggggaga
aaagtctgtttgcctcaggagtgtgaggactacactagtgaaagcgcctggcgggcagccggcgatgcccaataa
atgtgtgttttgctgtttgttaaaaaaaaaaaaaaaaa

FIG. 3A

SEQ ID NO:11

MPALCLVLCWFQGLLGEVWNAVDSGHCLQTYSLHTEAVRAARWAPCGRRILSGGFDFALHLTDLETGTQLFSGRS
DFRITTLKFHPKDHNIFLCGGFSSEMKAWDIRTGKVMRSYKATIQQTLDILFLREGSEFLSSTDASTRDSADRTI
IAWDFRTSAKISNQIFHERFTCPSLALHPREPVFLAQTNGNYLALFSTVWPYRMSRRRRYEGHKVEGYSVGCECS
PGGDLLVTGSADGRVLMYSFRTASRACTLQGHTQACVGTTYHPVLPSVLATCSWGGDMKIWH

FIG. 3B

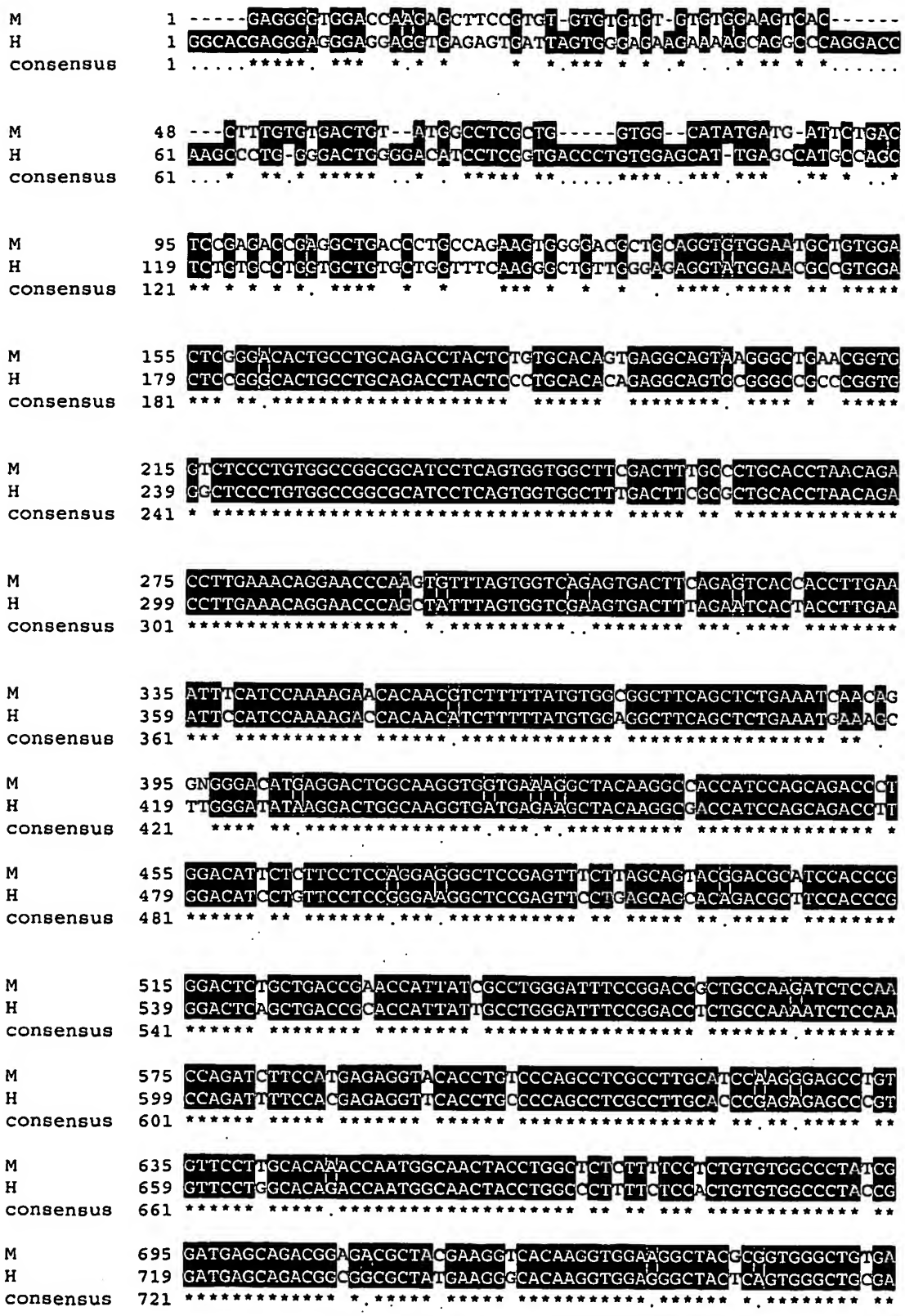

FIG. 4A

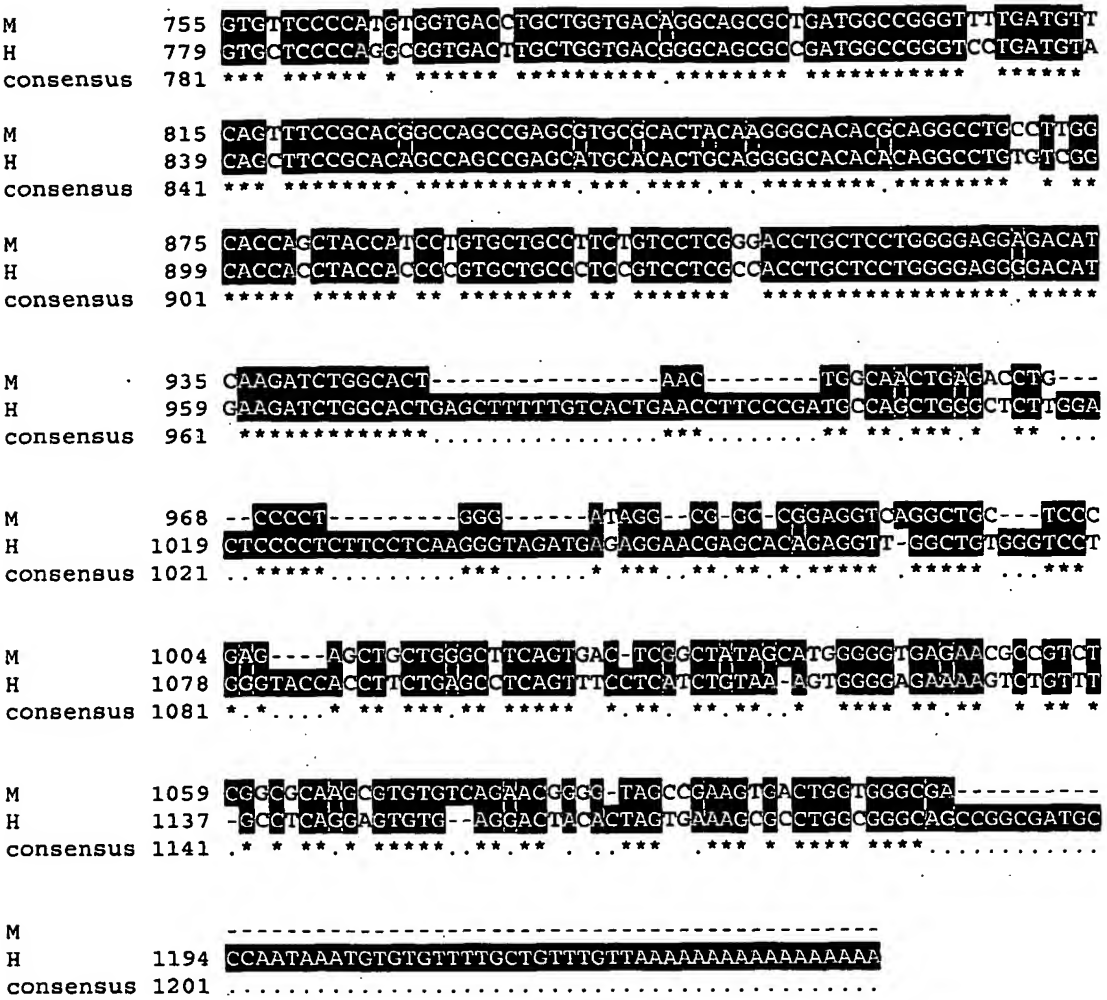

FIG. 4A (continued)


M 1 MMLLTPRPRLTLPEVGTLQVWNAVDSGHCLQTYSVHSEAVRAERWSPCGRRILSGGFDFA
H 1 --MPALCLVLCWFQGLLGEVWNAVDSGHCLQTYSLHTEAVRAARWAPCGRRILSGGFDFA
consensus 1 ... * ********** ****** ** **********
M 61 LHLTDLETGTQVFSGQSDFRVTTLKFHPKEHNVFLCGGFSSEINRXDMRTGKVVKGYKAT
H 59 LHLTDLETGTQLFSGRSDFRITTLKFHPKDHNIFLCGGFSSEMKAWDIRTGKVMRSYKAT
consensus 61 ********** **** ******** ********** ******
M 121 IQQTLDILFLQEGSEFLSSTDASTRDSADRTIIAWDFRTAAKISNQIFHERYTCPSLALH
H 119 IQQTLDILFLREGSEFLSSTDASTRDSADRTIIAWDFRTSAKISNQIFHERFTCPSLALH
consensus 121 ********** ********** ********
M 181 PREPVFLAQTNGNYLALFSSVWPYRMSRRRRYEGHKVEGYAVGCECSPCGDLLVTGSADG
H 179 PREPVFLAQTNGNYLALFSTVWPYRMSRRRRYEGHKVEGYSVGCECSPCGDLLVTGSADG
consensus 181 ********** ********** ******* **********
M 241 RVLMFSFRTASRACALQGHTQACLGTSYHPVLPSVLGTCSWGGDIKIWH
H 239 RVLMYSFRTASRACTLQGHTQACVGTIYHPVLPSVLATCSWGGDMKIWH
consensus 241 ****.********** ********.**.********.*******.****

FIG. 4B

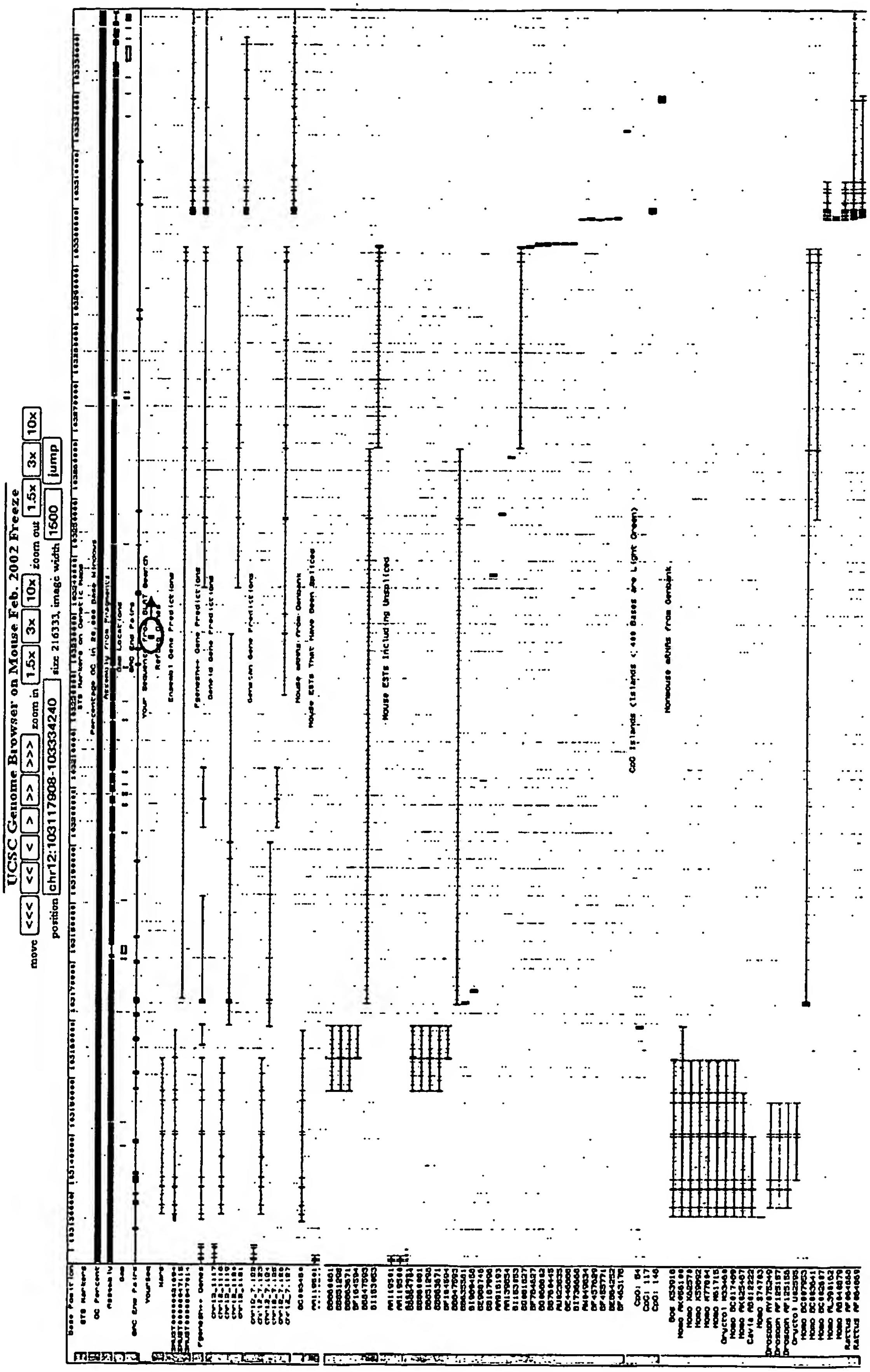
UCSC Genome Browser on Mouse Feb. 2002 Freeze
move <<< << < > >> >>> zoom in 1.5x 3x 10x zoom out 1.5x 3x 10x
position chr12:103117908-103334240 size 216333, image width 1600 jump

FIG.5A

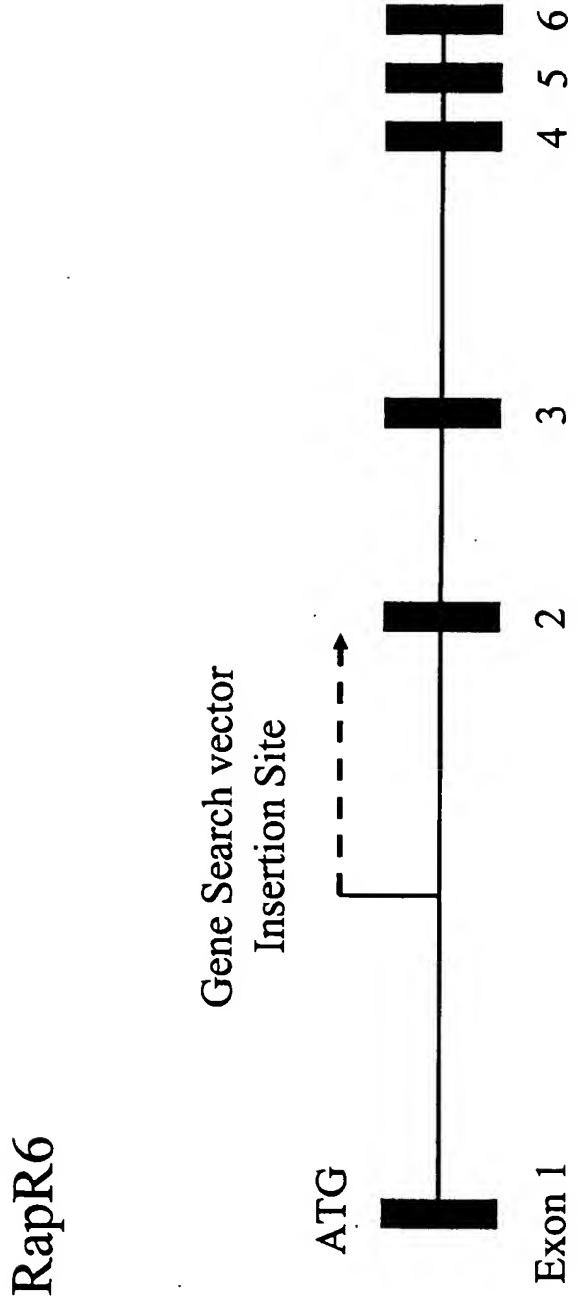

FIG. 5B

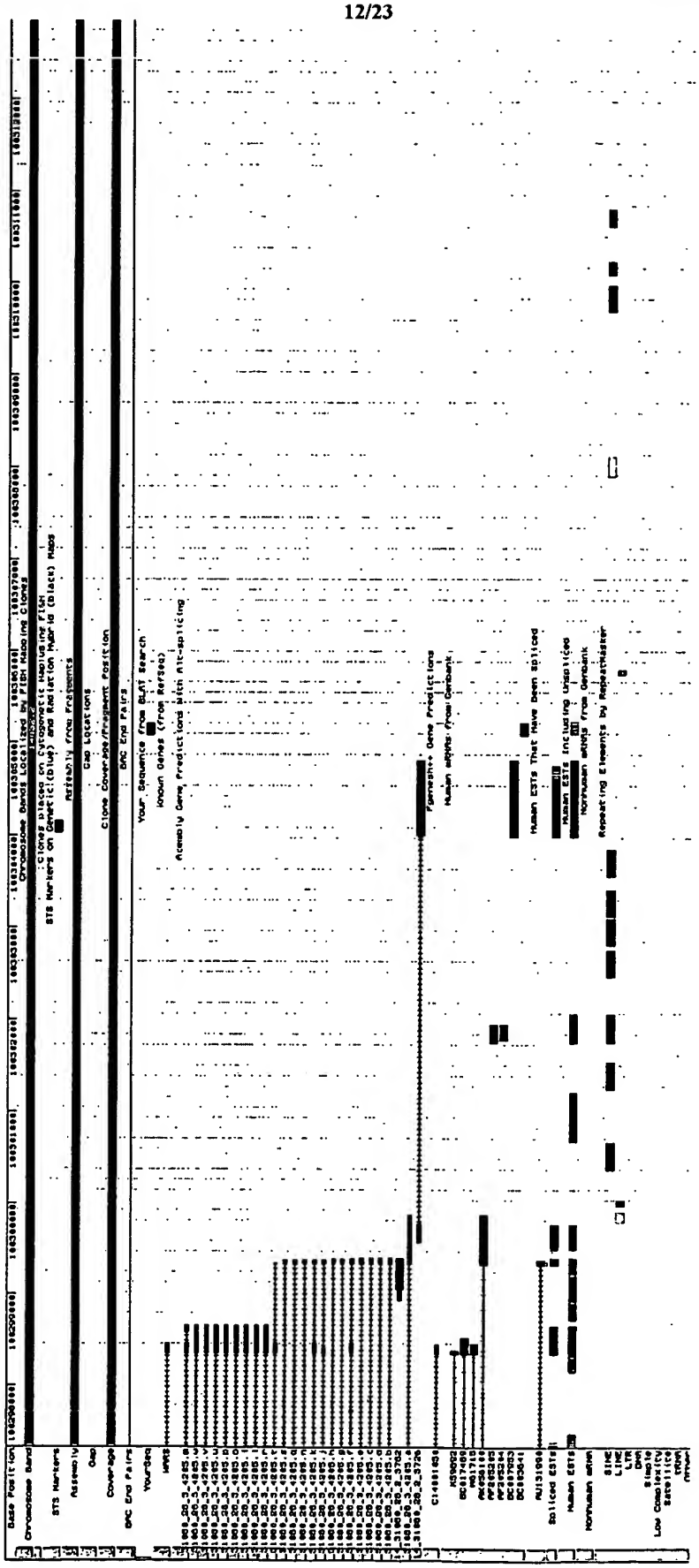
position chr14:100297347-100312946 size 15600, pixel width 1500 jump
Base Position
Chromosome Band
STS Markers
Assembly
Gap
Coverage
BAC End Pairs
Your Seq
mRNA
Human ESTs
Spliced ESTs
Human ESTs
Nonhuman mRNA
SINE
LINE
LTR
DNA
Simple
Low Complexity
Satellite
tRNA

FIG.6A

SMART

S imple
M odular
A rchitecture
R esearch
T ool

Reference Schultz et al. (1998) *Proc. Natl. Acad. Sci. USA* 95, 5857-5864
Letunic et al. (2002) *Nucleic Acids Res* 30, 242-244

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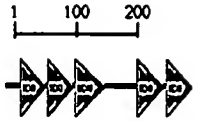
Currently there are too many SMART jobs running.

Your job is no. 1 in the queue.

Your sequence was 100% identical to sptrembl|Q9BTK5|Q9BTK5, displaying precalculated results.



Mouse over domain / undefined region to see the limits; click on it to go to further annotation; right-click to save whole protein as PNG image
Transmembrane segments as predicted by the *TMHMM2* program (▬), coiled coil regions determined by the *Coils2* program (—) and Segments of low compositional complexity, determined by the *SEG* program (—)

Architecture analysis

Display all proteins with similar domain organization.
Display all proteins with similar domain composition.

The SMART diagram above represents a summary of the results shown below. Domains with scores less significant than established cutoffs are not shown in the diagram. Features are also not shown when two or more occupy the same piece of sequence; the priority for display is given by SMART > PFAM > PROSPERO repeats > Signal peptide > Transmembrane > Coiled coil > Low complexity. In either case, features not shown in the above diagram are marked 'hidden'

Confidently predicted domains, repeats, motifs and features:

name	begin	end	E-value
signal peptide	1	17	-
WD40	24	63	4.30e-05
WD40	66	105	1.40e+00
WD40	108	154	1.90e+02
WD40	203	244	3.30e-01
WD40	247	287	2.90e-03

FIG.6B

```
2 possible models considered, only significant TM-segments used

*** the models differ in the number of TM-helices ! ***

------> STRONGLY prefered model: N-terminus inside
 2 strong transmembrane helices, total score : 1224
 # from   to length score orientation
 1    1   21 (21)     510 i-o
 2  210  232 (23)     714 o-i

------> alternative model
 1 strong transmembrane helices, total score : 812
 # from   to length score orientation
 1    6   25 (20)     812 o-i
```

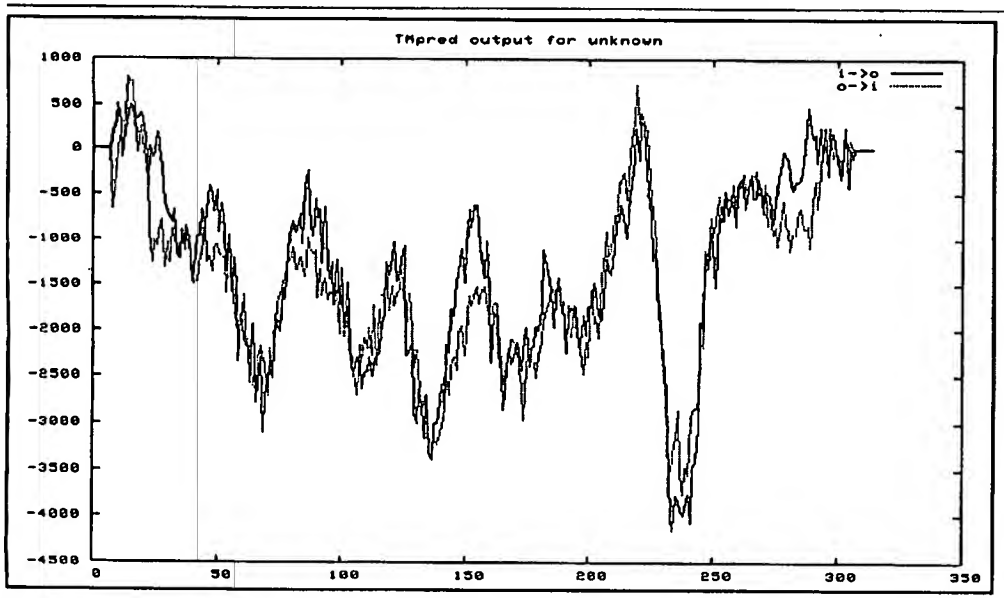


FIG.6C

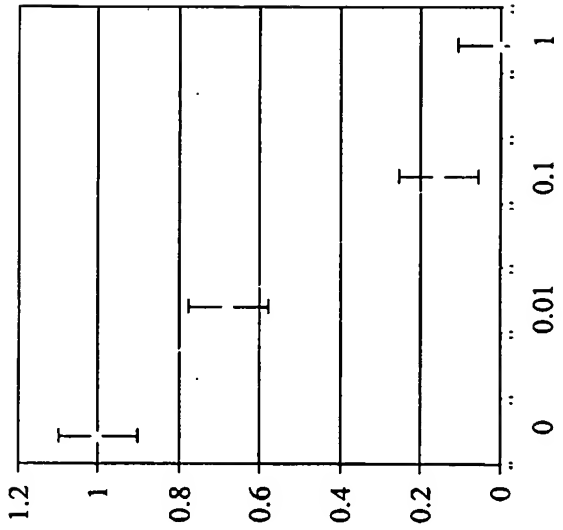


FIG. 7

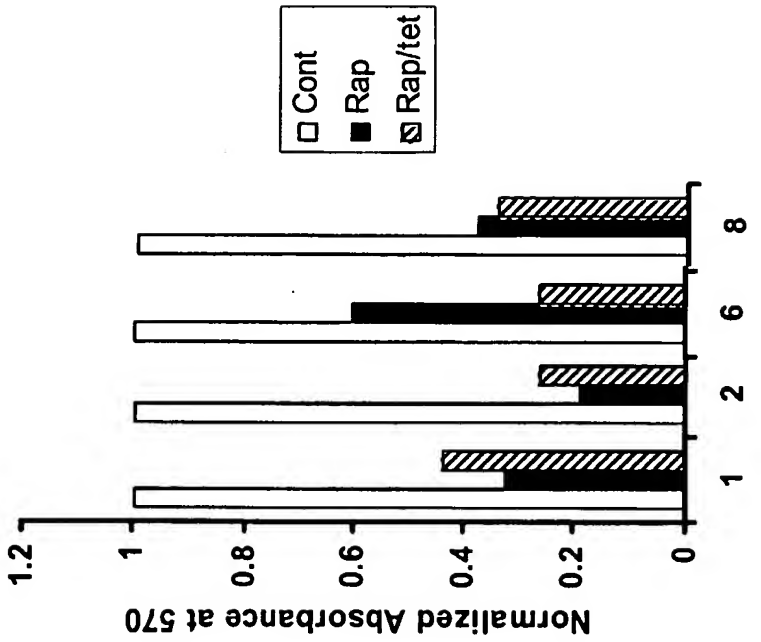

Cont
Rap
Rap/tet
Normalized Absorbance at 570
1.2
1
0.8
0.6
0.4
0.2
0
1
2
6
8

FIG. 8A

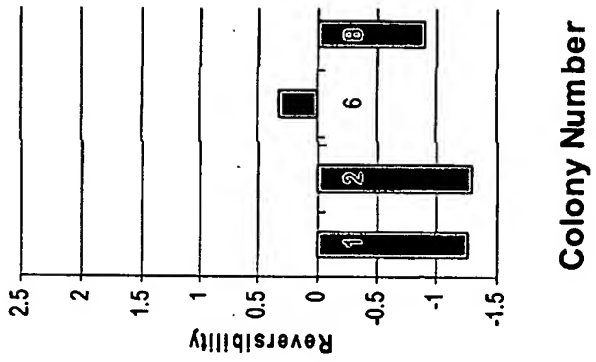


FIG. 8B

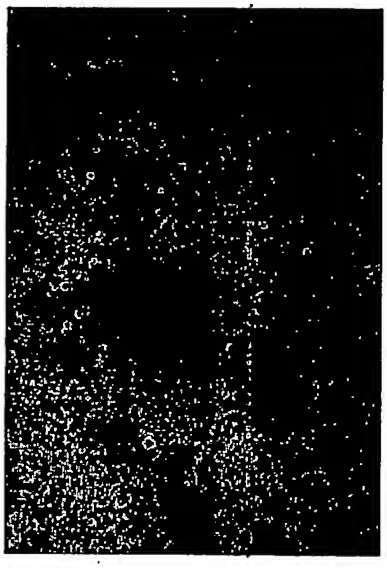


FIG. 8C

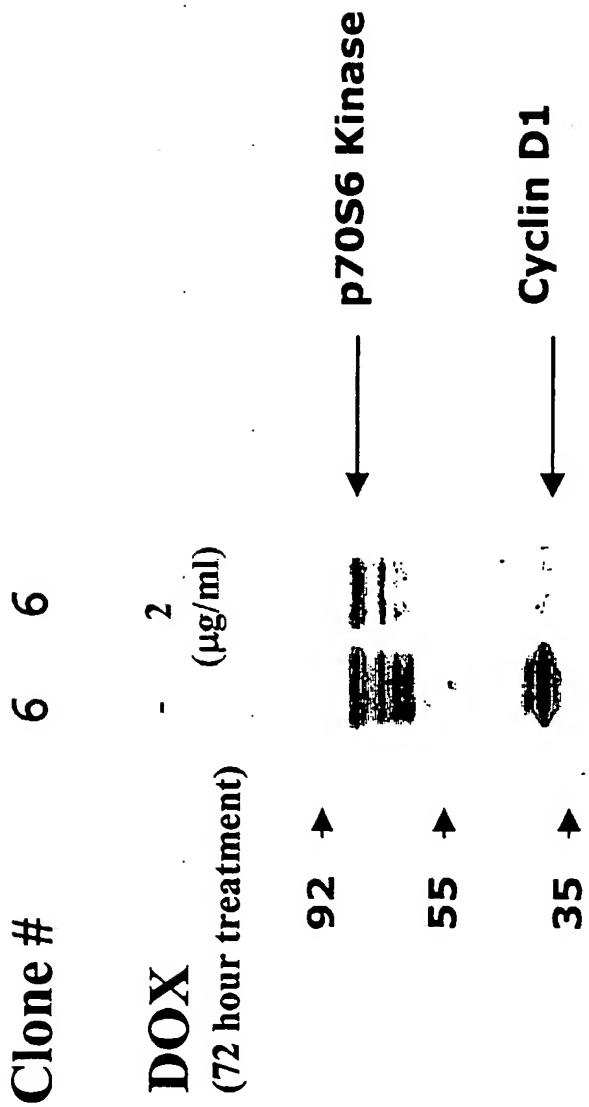

Clone #
6 6
DOX
(72 hour treatment)
- 2
(μg/ml)
92
55
35
p70S6 Kinase
Cyclin D1

FIG. 8D

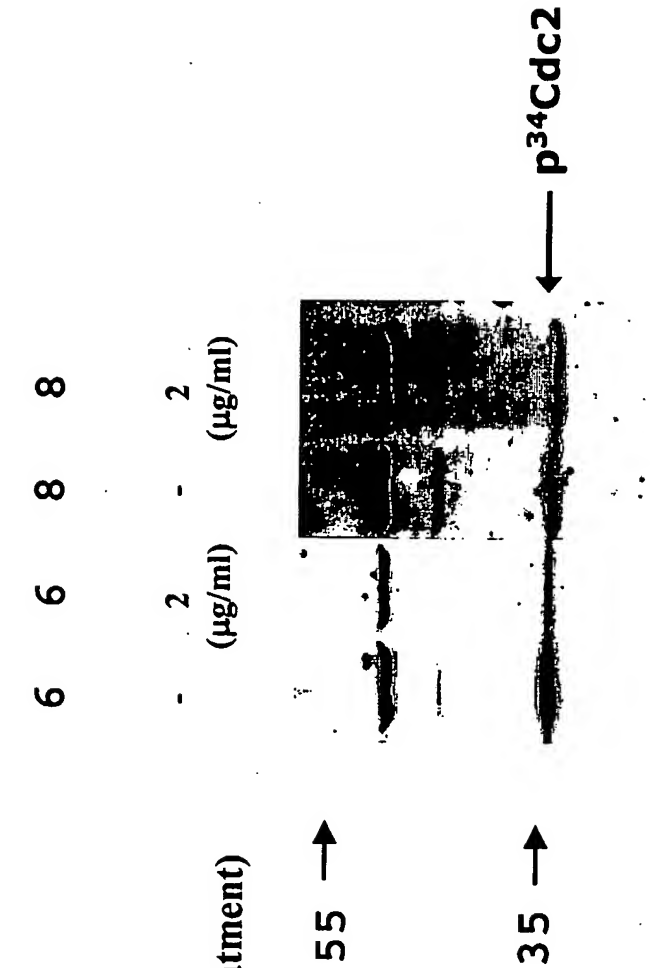


FIG. 8E


Ori-Cat
Tet-Regulated Promoter
Puro

FIG. 9A

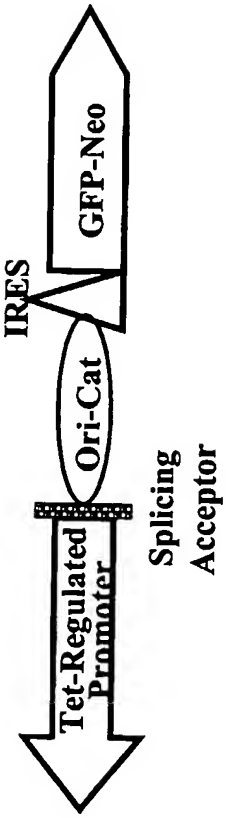

GFP-Neo
IRES
Ori-Cat
Splicing Acceptor
Tet-Regulated Promoter

FIG. 9B

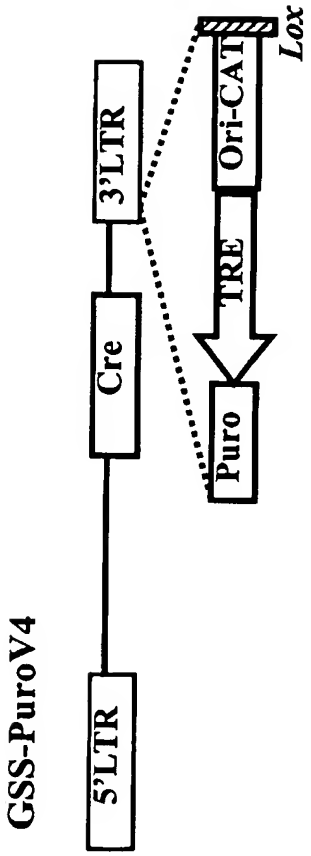

GSS-PuroV4
5'LTR
Cre
3'LTR
Puro
TRE
Ori-CAT
Lox

FIG. 9C

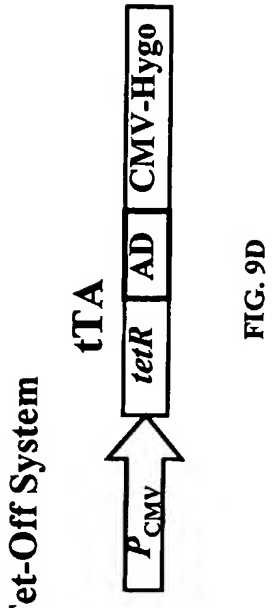

Tet-Off System
tTA
P_{CMV}
tetR
AD
CMV-Hygo

FIG. 9D

Accession class	Nucleotide accession	Nucleotide Position	Hit orientation	dbSNP rs# (cluster id)	Protein accession	Function
NCBI RefSeq	NM_024515.1	908	minus strand	rs13065	NP_078791.1	unclassified
		1192	minus strand	rs13492	NP_078791.1	unclassified
GenBank mRNA	BC003641.1	908	minus strand	rs13065	AAH03641.1	unclassified
		1192	minus strand	rs13492	AAH03641.1	unclassified

FIG.10